

BLASTP ALIGNMENT OF SEQ ID NO: 5 WITH ADIPONECTIN POLYPEPTIDE (SEQ ID NO: 402)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 5)  
 Subject: gi15213856 AF404407\_1 (AF404407) adiponectin [Macaca mulatta] (SEQ ID NO: 402)  
 Length = 243

Score = 158 (60.7 bits), Expect = 1.3e-08, P = 1.3e-08

Identities = 42/136 (30%), Positives = 67/136 (49%)

Query:	670	RVAFSAA-RTSNLAPGTL	QPIVFDLLNNLGETFDLQ	GRFNC	VPVNGTYVFIFHMLKLA	728
		R AFS	T P + PI F + N	+D	G+F+C + G Y F +H+	
Sbjct:	111	RSAFSVGLETYVTVP	--NMP	IRFTKIFYNQ	NHYDGTGK	FHCNIPGLYYFAYHITVYM 167
Query:	729	VNVPLYVNL	MKNEEVLVSAYANDGAPDHETASN	HAILQLFQGDQIWLRLH	----	RGAIYG 784
		+V	V+L K ++ ++ Y	+ + AS	+L L GDQ+WL+++ R +Y	
Sbjct:	168	KDVK--VSLFKDKKAMLF	TYDQYQENNVDQASGSVLLHLE	VGDVQVWLQVYGEGER	NGLYA	225
Query:	785	SSWKYSTFGYLLYQD	800			
		+ STF+G+LLY	D			
Sbjct:	226	DNDNDSTFTGFLLYHD	241			

FIG. 1

BLASTP ALIGNMENT OF SEQ ID NO: 5 WITH HUMAN ADIPONECTIN  
AMINO ACID SEQUENCE (SEQ ID NO: 404)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 5)  
Subject: AAY85144 13-MAR-2000 09-MAR-1999 20-JUN-2000 09-MAR-1999 Human  
adiponectin amino acid sequence. [Homo sapiens] (SEQ ID NO: 404)  
Length = 244

Score = 156 (60.0 bits), Expect = 4.3e-09, P = 4.3e-09

Identities = 41/136 (30%), Positives = 67/136 (49%)

Query: 670 RVAFSAA-RTSNLAPGTLDPVFDLLNNLGETFDLQGRFNCVPVNGTYVFIFHMLKLA 728  
R AFS T P + P F + N +D G+F+C + G Y F +H+

Sbjct: 112 RSAFSVGLETYTYTIP---NMPERFTKIFYNQNHYDGTGKFCNIPGLYYFAYHITVYM 168

Query: 729 VNVPLYVNLMKNEEVLSAYANDGAPDHETASNHAILQLFQGDQIWLRLH---RGAIYG 784  
+V V+L K ++ ++ Y +++ AS +L L GDQ+WL+++ R +Y

Sbjct: 169 KDVK--VSLFKDKKAMLFYDQYQENNYDQASGSVLLHLEVGQVWLQVYGEGERNGLYA 226

Query: 785 SSWKYSTFSGYLLYQD 800  
+ STF+G+LLY D

Sbjct: 227 DNDNDSTFTGFLLYHD 242

FIG. 2

BLASTP ALIGNMENT OF SEQ ID NO: 15 WITH ADIPONECTIN POLYPEPTIDE (SEQ ID NO: 402)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 15)  
 Subject: gi15213856 AF404407\_1 (AF404407) adiponectin [Macaca mulatta] (SEQ ID NO: 402)  
 Length = 243

Score = 147 (56.8 bits), Expect = 2.6e-07, P = 2.6e-07

Identities = 40/136 (29%), Positives = 65/136 (47%)

Query: 580 RFAFSAA-RTSNLAPGTLDPYGVDDLNNLGETFDLQGRFNCVPVNGTYVFIFHMLKLA 638

R AFS T P + P + N +D G+F+C + G Y F +H+

Sbjct: 111 RSFVSVGLETYVTVP---NMPIRFTKIFYNQNHVDGSGTGFHCNIPGLYFAYHITVYM 167

Query: 639 VNVPLYVNLKNEEVLSAYANDGAPDHETASNHAILQLFQGDQIWLRLH----RGAIYG 694

+V V+L K ++ ++ Y + + AS +L L GDQ+WL+++ R +Y

Sbjct: 168 KDVK--VSLFKDKKAMLFYDQYQENNVDQASGSVLLHLEVGQVWLQVYGEGERNGLYA 225

Query: 695 SSWKYSTFGYLLYQD 710

+ STF+G+LLY D

Sbjct: 226 DNDNDSTFTGFLLYHD 241

FIG. 3

BLASTP ALIGNMENT OF SEQ ID NO: 15 WITH HUMAN ADIPONECTIN  
AMINO ACID SEQUENCE (SEQ ID NO: 404)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 15)  
Subject: AAY85144 13-MAR-2000 09-MAR-1999 20-JUN-2000 09-MAR-1999 Human  
adiponectin amino acid sequence. [Homo sapiens] (SEQ ID NO: 404)  
Length = 244

Score = 151 (58.2 bits), Expect = 1.5e-08, P = 1.5e-08

Identities = 40/136 (29%), Positives = 66/136 (48%)

Query: 580 RVAFSAA-RTSNLAPGTLDPYGVDDLNNLGETFDLQGRFNCVPVNGTYVFIFHMLKLA 638  
R AFS T P + P + N +D G+F+C + G Y F +H+  
Sbjct: 112 RSAFSVGLETYTYTIP---NMPERFTKIFYNQNHYDGTGKFCNIPGLYYFAYHITVYM 168  
Query: 639 VNVPLYVNLKNEEVLSAYANDGAPDHETASNHAILQLFQGDQIWLRLH----RGAIYG 694  
+V V+L K ++ ++ Y +++ AS +L L GDQ+WL+++ R +Y  
Sbjct: 169 KDVK--VSLFKKDKAMLFTYDQYQENNYDQASGSVLLHLEVGQVWLQVYGEGERNGLYA 226  
Query: 695 SSWKYSTFSGYLLYQD 710  
+ STF+G+LLY D  
Sbjct: 227 DNDNDSTFTGFLLYHD 242

FIG. 4



BLASTP ALIGNMENT OF SEQ ID NO: 28 WITH HUMAN ADIPONECTIN  
AMINO ACID SEQUENCE (SEQ ID NO: 404)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 28)  
Subject: AAY85144 13-MAR-2000 09-MAR-1999 20-JUN-2000 09-MAR-1999 Human  
adiponectin amino acid sequence. [Homo sapiens] (SEQ ID NO: 404)  
Length = 244

Score = 363 (132.8 bits), Expect = 6.7e-33, P = 6.7e-33

Identities = 87/236 (36%), Positives = 129/236 (54%)

Query: 514 IPGPKGEPGLPGPPGFPFGIGKPGVAG-LHGPPGKPGALGPGQPGGLPGPPGPPGPPA 572  
+PG E + GP + K G + G PG PG G G+ G G PG G G P  
Sbjct: 13 LPGHDQETTIQPGVLLPLPKGACTGWMAGIPGHPGHNGAPGRDGRDGTGKEKGDGP 72

Query: 573 VMPPTPPPGGEYLPDMG-LGIDGVKPPHAYGAKKNGGP---AYEM-PAFTAELTAPFP 627  
++ P +G D+G G+ G + P + +G+ G P AY AF+ L +  
Sbjct: 73 LIGP-----KG----DIGETGVPGAEGPRGFPFGIQRKGEGEGAYVYRSAFSVGLETYT 124

Query: 628 PVGAPVKFNKLLYNGRQYNPQTGIFTCEVPGVYFYHVKGGNVWVALFKNNEPVMY 687  
P +F K+ YN + +Y+ TG F C +PG+YFYFYH+ +V V+LFK ++ +++  
Sbjct: 125 IPNMPERTKIFYNQNHVDGSTGKFHCNIPGLYFYFAYHITVYMKDVKVSFLFKDKAMLF 184

Query: 688 TYDEYKKGFLDQASGSVLLLRPGDRVFLQMPSE-QAAGLYAGQYVHSSFSGYLLY 742  
TYD+Y++ DQASGS +L L GD+V+LQ+ E + GLYA S+F+G+LLY  
Sbjct: 185 TYDQYQENNYDQASGSVLLHLEVGDVWLQVYGEGERNGLYADNDNDSTFTGFLLY 240

FIG. 6

BLASTP ALIGNMENT OF SEQ ID NO: 160 WITH ADIPONECTIN POLYPEPTIDE (SEQ ID NO: 402)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 160)  
 Subject: gi15213856 AF404407\_1 (AF404407) adiponectin [Macaca mulatta] (SEQ ID NO: 402)  
 Length = 243

Score = 410 (149.4 bits), Expect = 5.3e-38, P = 5.3e-38

Identities = 92/228 (40%), Positives = 133/228 (58%)

Query: 53 GPHGRIGLPGRDGRDGRKGEKGTAGLRGKTGPLGLAGEKGDQGETGKKGPIGPEGK 112  
 GP + LP G G G G+ G+ G G GEGG++G+ G IGP+G+

Sbjct: 23 GPGVLLPLPKGACTGWMAGIPGHPGHNVPGRDGRDGTGEGKEKGDPL---IGPKGDT 79

Query: 113 GEVGPIGPPGPKGDRGEQGDPLPGVCRCGSIVLKSAFSVGITTSYPEERLPIIFNKVLF 172  
 GE G G GP+G G QG G PG G+ V +SAFSVG+ T +PI F K+ +

Sbjct: 80 GETGVTGAEGPRGFPPIQGRKGEPE---GAYVRSAFSVGLETYTVTPNMPPIRFTKIFY 136

Query: 173 NEGEHYNPATGKFCAPGIIYFYSYDITLANKHLAIGLVHNGQYRIKTFDANTGNH-DVA 231  
 N+ HY+ +TGKF C PG+YF+Y IT+ K + + L + + T+D N+ D A

Sbjct: 137 NQQNHYDGSTGKFCNIPGLIYFAYHITVYMKDKVSLFKKOKAMLFYDQYQENNVDDQA 196

Query: 232 SGSTVIYLPQDEVWLEIFFT-DQNGLFSDPGWADSLFSGFLLYVDT 278

Sbjct: 197 SGSVLLHLEVGQVWLQVYGEGERNGLYADND-NDSTFTGFLLYHDTN 243

FIG. 7





BLASTP ALIGNMENT OF SEQ ID NO: 186 WITH ADIPONECTIN POLYPEPTIDE (SEQ ID NO: 402)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 186)  
 Subject: gi15213856 AF404407\_1 (AF404407) adiponectin [Macaca mulatta] (SEQ ID NO: 402)  
 Length = 243

Score = 472 (171.2 bits), Expect = 1.4e-44, P = 1.4e-44

Identities = 104/204 (50%), Positives = 130/204 (63%)

Query: 86 GIKGDQSGRSGPGKHGPKGLAGPMGEKGLRGETGPQGQGNKGDVGTGPEGPRGNIGPL 145

GI G G G PG+ G G GEKG G GP KG+ G+ G TG EGPRG G

Sbjct: 41 GIPGHPGHNGVPGRDGRTGPEKGEKGDPLIGP---KGDGTGTGTGAEGPRGFPGIQ 97

Query: 146 GPTGLPGPMGPICKPG-PKG-EAGPTGPQDMPKFDKILYNEFNHYDTAAGKFTCHIAGV 203

G G PG + + G E T P +MPI+F KI YN+ NHYD + GKF C+I G+

Sbjct: 98 GRKGEPGEGAYVYRSAFSVGLETYVTVP-NMPIRFTKIFYNQNHNDGSGTKFHCNIPGL 156

Query: 204 YYFTYHITVFSRNVQVSLVKNQVILHTKDAYMSSE-DQASGGIVLQLKLGDEVWLQVTG 262

YYF YHITV+ ++V+VSL K +L T D Y + DQASG ++L L++GD+VWLQV G

Sbjct: 157 YYFAYHITVYMKDVKVSFLFKDKAMLFYDQYQENNVDDQASGVSLLHLEVGQVWLQVYG 216

Query: 263 -GERFNGLFADEDDDTTFTGFLLF 285

GER NGL+AD D+D+TFTGFLL+

Sbjct: 217 EGER-NGLYADNDNDSTFTGFLLY 239

FIG. 9

BLASTP ALIGNMENT OF SEQ ID NO: 186 WITH HUMAN ADIPONECTIN  
AMINO ACID SEQUENCE (SEQ ID NO: 404)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 186)  
Subject: AAY85144 13-MAR-2000 09-MAR-1999 20-JUN-2000 09-MAR-1999 Human  
adiponectin amino acid sequence. [Homo sapiens] (SEQ ID NO: 404)  
Length = 244

Score = 458 (166.3 bits), Expect = 7.6e-44, P = 7.6e-44

Identities = 102/204 (50%), Positives = 129/204 (63%)

Query: 86 GIKDQSGRSGPGKHGPKGLAGPMGEKGLRGETGPQGQKGNKGDVGTGPEGPRGNIGPL 145  
GI G G G+PG+ G G G GEKG G GP KG+ G+ G G EGPRG G  
Sbjct: 42 GIPGHPGHNAGPRDGRDGTGPEKGEKGDPLIGP---KGDIGETGVPGAEGPRGFPGIQ 98

Query: 146 GPTGLPGPMGPICKPG-PKG-EAGPTGPQDMPKFKILYNEFNHYDTAAGKFTCHIAGV 203  
G G PG + + G E T P +MP +F KI YN+ NHYD + GKF C+I G+  
Sbjct: 99 GRKGPEGEGAYVYRSAFSVGLETTYTIP-NMPEFTKIFYNQNNHYDGTGKFCNIPGL 157

Query: 204 YYFTYHITVFSRNQVSLVKNVGVKILHTKDAYMSSE-DQASGGIVLQLKLGDEVWLQVTG 262  
YYF YHITV+ ++V+VSL K +L T D Y + DQASG ++L L++GD+VWLQV G  
Sbjct: 158 YYFAYHITVYMKDVKSFLFKDKAMLFYDQYQENNYDQASGSVLLHLEVGDVWLQVYG 217

Query: 263 -GERFNGLFADEDDDTTFTGFLLF 285  
GER NGL+AD D+D+TFTGFLL+  
Sbjct: 218 EGER-NGLYADNDNDSTFTGFLLY 240

FIG. 10

BLASTP ALIGNMENT OF SEQ ID NO: 215 WITH ADIPONECTIN POLYPEPTIDE (SEQ ID NO: 402)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 215)  
 Subject: gi15213856 AF404407\_1 (AF404407) adiponectin [Macaca mulatta] (SEQ ID NO: 402)  
 Length = 243

Score = 208 (78.3 bits), Expect = 1.4e-16, P = 1.4e-16

Identities = 57/178 (32%), Positives = 86/178 (48%)

Query: 104 GLAGPMGEKGLRGETGPQGGQGNKGDVPTGPEGRNIGLPTGLPGMPGPIGKPGPK 163  
G+ G G G+ G G G G KG+ G G GP+G+ G G TG GP G G G K

Subjct: 41 GTPGHPCHNGVPRDGRDGTPEGKEGKDPGLIGKPGTGTGTGTAEGPRGFPFGIQRK 100

Query: 164 GEAGTGPQGEFQVR-GIRGWKGRGEKGKIGETLVLPKSAFTVGLTVLSKFPSSDVPIK 222  
GE G G+ + + + + G T K F + +  
Subject: 101 GEPFGAYVRSAFSVGLETYVTVPNPIRFTKIFYNOQNHYD-GST--GKFKHCNIPGLY 157

Query: 223 FDKTHITVFSRNVQVSLVKNVGVKILHTRDAYVSSSE-DQASGSIVLQLKLGDEMWCVIH 279  
+ HITV+ ++V+VSL K +L T D Y + DQASGS++L L++GD++W ++

Spbict: 158 YFAXHITVYMKDVKVSFLFKKDKAMLFYDQYQENNVDQASGSVLLHLEVGQDQWLVQVY 215

FIG. 11

BLASTP ALIGNMENT OF SEQ ID NO: 215 WITH HUMAN ADIPONECTIN  
 AMINO ACID SEQUENCE (SEQ ID NO: 404)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 215)  
 Subject: AAY85144 13-MAR-2000 09-MAR-1999 20-JUN-2000 09-MAR-1999 Human  
 adiponectin amino acid sequence. [Homo sapiens] (SEQ ID NO: 404)  
 Length = 244

Score = 213 (80.0 bits), Expect = 7.0e-18, P = 7.0e-18

Identities = 60/182 (32%), Positives = 91/182 (50%)

Query: 104 GLAGPMGEKGLRGETGPQKGKNGKDVGPTGPEGPRGNIGPLGPTGLPGMGPIGKPGPK 163  
 G+ G G G G G G G KG+ G G GP+G+IG TG+PG GP G PG +  
 Sbjct: 42 GIPGHPCHNGAPGRDGRDGTGPKGKGKGDPLIGPKGDIGE---TGVPGAEGPRGFPGIQ 98

Query: 164 GEAGPTGPQGEPGVR-----GIRGWKGDGRGKIGETLVLPKSAFTVGLTVLSKFPSSD 218  
 G G G +G R G+ + + + ++ + G T KF +  
 Sbjct: 99 GRKGEPG-EGAYVYRSAFSVGLETTYTIPNMPERFTKIFYNQNHVD-GST--GKFHCNI 154

Query: 219 VPIKFDKIHIITVFSRNVQVSLVKNVGKILHTRDAYVSSE-DQASGSIVLQLKLGDEMWCV 277  
 + + HITV+ ++V+VSL K +L T D Y + DQASGS++L L++GD++W  
 Sbjct: 155 PGLIYFAYHITVYMKDVKVSFLFKDKKAMLFITYDQYQENNYDQASGSVLLHLEVGQVWLQ 214

Query: 278 IH 279  
 ++  
 Sbjct: 215 VY 216

FIG. 12

## BLASTP ALIGNMENT OF SEQ ID NO: 241 WITH ADIPONECTIN POLYPEPTIDE (SEQ ID NO: 402)

Sbjct: 219 ER-NGLYADNDNDSTFTGFLLY 239

FIG. 13

BLASTP ALIGNMENT OF SEQ ID NO: 241 WITH HUMAN ADIPONECTIN  
AMINO ACID SEQUENCE (SEQ ID NO: 404)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 241)  
 Subject: AAY85144 13-MAR-2000 09-MAR-1999 20-JUN-2000 09-MAR-1999 Human  
 adiponectin amino acid sequence. [Homo sapiens] (SEQ ID NO: 404)  
 Length = 244

Score = 473 (171.6 bits), Expect = 2.0e-45, P = 2.0e-45

Identities = 100/202 (49%), Positives = 128/202 (63%)

**Query:** 131 GPTPEGPRGNIGPLPTGLPGMPPIKGPKGEAGTCTPQCEPVQGIRGWKGDGRGEK 190  
G G G G G G G G G G G G G G G G G + G + G K

**Sbjct:** 42 GTPGHPGHNGAPGRDRDGTPEKEKGKDGPLIGPKGDIGETCTVPGAEGPRGFPGIQRK 101

Query: 191 GKIGETLVLPKSAFTVGLTVLSKFPSSDRPIKFDKILYNEFNHYDTAAGKFTCHIAGVY 250  
G+ GE + +SAF+VGL P+ P +F KI YN+ NHYD + GKF C+I G+YY

sbjct: 102 GEPEGAXVRSAFSVGLETTYTIPNM--PERFTKIFVNOQNHYDVGSTGKFKHCNIPGLYY 159

Query: 251 FTYHITVFSRNQVSLVKNQVKILHTKDAYMSSE-DQASGGIVLQKLGDDEVWLQVTG-G 308  
F YHITV+ ++V+VSL K +L T D Y + DQASG ++L L++GD+VWLQV G G

Subject: 160 FAYHITVYMKDVKSFLKKDKAMLFYDQYQENNYDQASGSVLLHLEVGDDQVWLQVYGE 219

Query: 309 ERFNGLFADEDDDTTFTGFLLF 330  
ER NGL+AD D+D+TFTGFL+  
Subject: 220 ER-NGLYADNDNDSTFTGFLLY 240

FIG. 14

BLASTP ALIGNMENT OF SEQ ID NO: 272 WITH  
ADIPOSE TISSUE-SPECIFIC PROTEIN ADIPO Q (SEQ ID NO: 403)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 272)  
Subject: gi14289336 AF269230\_1 (AF269230) adipose tissue-specific protein adipon Q  
[Bos taurus] (SEQ ID NO: 403) Length = 240

Score = 212 (79.7 bits), Expect = 1.0e-34, Sum P(2) = 1.0e-34

Identities = 41/78 (52%), Positives = 56/78 (71%)

Query: 227 HITVFSRNVQVSLVKNQVILHTKDAYMSSE-DQASGGIVLQLKLGDEVVLQVTGGERFN 285  
HITV+ ++V+VSL K +L T D Y DQASG ++L L++GD+VWLQV GE N  
Sbjct: 158 HITVYMKDVKVSFLFKKDKAVLFTYDQYQEKNVQASGSVLLHLEVGQVWLQVYEGENHN 217

Query: 286 GLFADEDDTTFTGFLLF 303  
G++AD +D+TFTGFLL+  
Sbjct: 218 GYADNVNDSTFTGFLLY 235

FIG. 15a

BLASTP ALIGNMENT OF SEQ ID NO: 272 WITH  
ADIPOSE TISSUE-SPECIFIC PROTEIN ADIPO Q (SEQ ID NO: 403)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 272)  
Subject: gi14289336 AF269230\_1 (AF269230) adipose tissue-specific protein adipo Q  
[Bos taurus] (SEQ ID NO: 403) Length = 240

Score = 183 (69.5 bits), Expect = 1.0e-34, Sum P(2) = 1.0e-34

Identities = 43/100 (43%), Positives = 56/100 (56%)

Query: 6 LLLAIEICTGNINSQD-----TCRQHPGIPGNPGHNGLPGRDGRDGAKGDKGDAGEPG 59  
LLLA+ G N +D C GIPG+PGHNG PGRDGRDG G+KG+ G+ G  
Sbjct: 9 LLLALP-SHGEDNMEDPPLPKGACAGWMAGIPGHPGHNGTTPGRDGRDGTTPGKGEKGDAG 67

Query: 60 RPSGPGKDGTSGEKGERGADGKVEAKGIKGDQGSRGSPGK 99  
G G+ +G+ G GA+G +G G G +G PG+  
Sbjct: 68 LLGPKGE---TGDVGMTGAEGP---RGFPPTPRKKEPGE 101

FIG. 15b





BLASTP ALIGNMENT OF SEQ ID NO: 302 WITH ADIPONECTIN POLYPEPTIDE (SEQ ID NO: 402)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 302)  
 Subject: gi15213856 AF404407\_1 (AF404407) adiponectin [Macaca mulatta] (SEQ ID NO: 402)  
 Length = 243

Score = 330 (121.2 bits), Expect = 1.6e-29, P = 1.6e-29

Identities = 82/220 (37%), Positives = 116/220 (52%)

Query: 124 PSTAATPDRGLMQSLPTFIQPKGEAGRPKGAGPRGPPGEPGPPGMPGPPGKEGEPGRQG 183

P A T G M +P G G GR G+ G G GE G PG +GP G+ GE G G  
 Sbjct: 31 PKGACT---GWMAGIPGH-PGHNGVPGRDGRDGTGPKGKEGKDPGLIGPKGDTGETGTG 86

Query: 184 LPPPPGAPGLNAA-GAISAATYSTGPKIAFYAGLKRQHEGYEV-LKFDDVVVTLGNHYDP 241

GP G PG+ G Y + AF GL+ + ++F + N NHYD  
 Sbjct: 87 AEGPRGFPGIQGRKGEPEGAYVY--RSAFSVGLETYTVTPNMPIRFTKIFYNQNHYDG 144

Query: 242 TTGKFTCSIPGIYFFTYHVLMRGGDGTSMWADLCKNNQVRASIAQADQNYDYASNSVV 301

+TGKF C+IPG+Y+F YH+ + D + L K ++ Q + N D AS SV+  
 Sbjct: 145 STGKFHCNIPGLYYFAYHITVYMKD--VKVSLFKKDKAMLFYDQYQENNVVDQASGVL 201

Query: 302 LHLEPGDEVYIKLDG-GKAHG--GNNNKYSTFSGFIIYAD 338

LHLE GD+V++++ G G+ +G +N+ STF+GF++Y D  
 Sbjct: 202 LHLEVGQDQVWLQVYGEGERNGLYADNDNDSTFTGFLLYHD 241

FIG. 17

BLASTP ALIGNMENT OF SEQ ID NO: 302 WITH HUMAN ADIPONECTIN  
AMINO ACID SEQUENCE (SEQ ID NO: 404)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 302)  
Subject: AAY85144 13-MAR-2000 09-MAR-1999 20-JUN-2000 09-MAR-1999 Human  
adiponectin amino acid sequence. [Homo sapiens] (SEQ ID NO: 404)  
Length = 244

Score = 336 (123.3 bits), Expect = 5.8e-31, P = 5.8e-31

Identities = 83/220 (37%), Positives = 117/220 (53%)

Query: 124 PSTAATPDRGLMQSLPTFIQGPKEAGRPKGAGPRGPPGPPGPPGKEKGEGRQG 183  
P A T G M +P G G GR G+ G GE G PG +GP G+ GE G G  
Sbjct: 32 PKGACT--GWMAGIPGH-PGHNGAPGRDGRDGTGPEKGEKGDPLIGPKGDIGETGVP 87

Query: 184 LPPPGAPGLNAA-GAISAATYSTGPKIAFYAGLKRQHEGYEVL-KFDDVVTNLGNHYDP 241  
GP G PG+ G Y + AF GL+ + + +F + N NHYD  
Sbjct: 88 AEGPRGFPGIQGRKGEPEGAYVY--RSAFSVGLETTYITIPNMPERFTKIFYNQNHYDG 145

Query: 242 TTGKFTCSIPGIYFFTYHVMRGGDGTSMWADLCKNNQVRASIAQDADQNYDYASNSVV 301  
+TGKF C+IPG+Y+F YH+ + D + L K ++ Q + NYD AS SV+  
Sbjct: 146 STGKFHCNIPGLYYFAYHITVYMKD---VKVSLFKKDKAMLFITYDQYQENNYDQASGSVL 202

Query: 302 LHLEPGDEVYIKLDG-GKAHG--GNNNKYSTFSGFIIYAD 338  
LHLE GD+V++++ G G+ +G +N+ STF+GF++Y D  
Sbjct: 203 LHLEVGQVWLQVYGEGERNGLYADNDNDSTFTGFLLYHD 242

FIG. 18

BLASTP ALIGNMENT OF SEQ ID NO: 323 WITH ADIPONECTIN POLYPEPTIDE (SEQ ID NO: 402)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 323)  
 Subject: gil5213856 AF404407\_1 (AF404407) adiponectin [Macaca mulatta] (SEQ ID NO: 402)  
 Length = 243

Score = 330 (121.2 bits), Expect = 1.6e-29, P = 1.6e-29

Identities = 82/220 (37%), Positives = 116/220 (52%)

Query: 30 PSTAATPDRGLMQSLPTFIQPKGEAGRPGKAGPRGPPGEPGPPGPMGPPGKEGEPGRQG 89

P A T G M +P G G GR G+ G G GE G PG +GP G+ GE G G  
 Sbjct: 31 PKGACT--GWMAGIPGH-PGHNGVPGRDGRDTPGKEGKEGKDPGLIGPKGDTGETGTG 86

Query: 90 LPPPGAPGLNAA-GAISAATYSTGPKIAFYAGLKRQHEGYEV-LKFDDVVVTNLGNHYDP 147

GP G PG+ G Y + AF GL+ + ++F + N NHYD  
 Sbjct: 87 AEGPRGFGIQRKGEPEGAYVY--RSAFVSGLETYYTVPNMPIRFTKIFYNQNHYDG 144

Query: 148 TTGKFTCSIPGIYFFYYHVMRGGDGTSMWADLCKNNQVRASAIQAQADQNYDYASNSVV 207

+TGKF C+IPG+Y+F YH+ + D + L K ++ Q + N D AS SV+  
 Sbjct: 145 STGKFHCNIPGLYYFAYHITVYMKD--VKVSLFKKDKAMLFTYDQYQENNVDDQASGVL 201

Query: 208 LHLEPGDEVYIKLDG-GKAHG--GNNNKYSTFSGFIIYAD 244

LHLE GD+V++++ G G+ +G +N+ STF+GF++Y D  
 Sbjct: 202 LHLEVGQDQVWLQVYGEGERNGLYADNDNDSTFTGFLLYHD 241

FIG. 19



BLASTP ALIGNMENT OF SEQ ID NO: 348 WITH ADIPONECTIN POLYPEPTIDE (SEQ ID NO: 402)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 348)  
 Subject: gi15213856 AF404407\_1 (AF404407) adiponectin [Macaca mulatta] (SEQ ID NO: 402)  
 Length = 243

Score = 138 (53.6 bits), Expect = 1.9e-06, P = 1.9e-06

Identities = 69/220 (31%), Positives = 90/220 (40%)

Query: 296 PQPPGSTGVIAETGQAGPPAGAGVSGR-GLPRGVDGQTGSGTVPGAEGFAGAPGYPKSPP 354  
 P PG GV G+ G P G G GL G G TG V GAEG G PG

Sbjct: 43 PGHPGHNGVPGRDGRDGTGEGKEKGDPLI-GPKGDTGETGTGAEGPRGFPGIQGRKG 101

Query: 355 VASPGAPVPSLVFSAGL-TQKPFPSDGGVVLFNKVLVNDGDVYNPSTGVFTAPYDGRYL 413  
 GA V +FS GL T P+ + F K+ N + Y+ STG F G Y

Sbjct: 102 EPEGAYVYRS-AFSVGLETYYTVPNMP--IRFTKIFYNQNHYDGTGKFKHCNIPGLYY 158

Query: 414 ITATLTPERDAYVEAV-LSVSNASVAQLHTAGYRREFLEYHRPTGALHTCGPGAFHLIV 472  
 +T Y++ V +S+ A L T Y + ++ G +++

Sbjct: 159 FAYHIT----VYMKDVKVSFLFKDKAMLFT--Y-----DQYQENNVDAQSGS-----VLL 202

Query: 473 HLKAGDAVNVVVTG-----GKLAHTDFDEMYSTFSGVFLY 507  
 HL+ GD V + V G G A D D STF+G LY

Sbjct: 203 HLEVGDQVWLQVYGEGERNGLYADNDND---STFTGFLLY 239

FIG. 21

BLASTP ALIGNMENT OF SEQ ID NO: 348 WITH HUMAN ADIPONECTIN  
 AMINO ACID SEQUENCE (SEQ ID NO: 404)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 348)  
 Subject: AAY85144 13-MAR-2000 09-MAR-1999 20-JUN-2000 09-MAR-1999 Human  
 adiponectin amino acid sequence. [Homo sapiens] (SEQ ID NO: 404)  
 Length = 244

Score = 132 (51.5 bits), Expect = 1.7e-06, P = 1.7e-06

Identities = 75/243 (30%), Positives = 98/243 (40%)

Query: 269 PRPSGPATAEDPGRRPVLPQRPPEERPQPQPGSTGVIAETQAGPPAGAGVSGRGLPRGV 328  
 P P G T G +P P P G G E G+ G P G+ G P+G  
 Sbjct: 30 PLPKGACTGWMAG----IPGHPGHNGAPGRDGRDTPGKGEKGDG---GLIG---PKGD 79

Query: 329 DGQTGSGTVPGAEGFAGAPGYPKSPVPASPAPVPSLVFSAGL-TQKPFPSDGGVVLFN 387  
 G+TG VPGAEG G PG GA V +FS GL T P+ F  
 Sbjct: 80 IGETG---VPGAEGPRGFPFGIQGRKGEPEGAYVYRS-AFSVGLETYYTIPNMPE--RFT 133

Query: 388 KVLVNDGDVYNPSTGVFTAPYDGRYLITATLTPERDAYVEAV-LSVSNASVAQLHTAGYR 446  
 K+ N + Y+ STG F G Y +T Y++ V +S+ A L T  
 Sbjct: 134 KIFYNQONHYDGSTGKFHCNIPGLYYFAYHIT----VYMKDVKVSFLFKDKAMLFYDQY 189

Query: 447 REFLEYHRPTGA--LHTCGGPGAFHLIVHLKAGDAVNVVTTGGKLAHTDFDEMYSTFSGV 504  
 +E Y + +G+ LH G + L V+ G+ G A D D STF+G  
 Sbjct: 190 QEN-NYDQASGSVLLHLEVGQVW-LQVY---GEGE-----NGLYADNDND---STFTGF 237

Query: 505 FLY 507  
 LY  
 Sbjct: 238 LLY 240

FIG. 22

BLASTP ALIGNMENT OF SEQ ID NO: 355 WITH ADIPONECTIN POLYPEPTIDE (SEQ ID NO: 402)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 355)  
 Subject: gil5213856 AF404407\_1 (AF404407) adiponectin [Macaca mulatta] (SEQ ID NO: 402)  
 Length = 243

Score = 199 (75.1 bits), Expect = 1.2e-15, P = 1.2e-15

Identities = 53/134 (39%), Positives = 68/134 (50%)

Query:	37	PRGPGPDGAPASVPPFP-----PGAKGEVRRGKAGLRGPPGPPGPRGPPGEPGRPGPPG	91
		P+G G A +P P PG G G G+ G +G PG GP+G GE G G G	
Sbjct:	31	PKG-ACTGWMAGIPGHPGHNGVPGRDGRDGTGPKGKGDPLIGPKGDTGETGTGAEG	89
Query:	92	PPG-PGPGGVA--PAAG-YVPRIAFYAGLRRRPHEGYEV-LRFDDVVTNVGNAYEAAAGKF	146
		P G PG G P G YV R AF GL + +RF + N N Y+ ++GKF	
Sbjct:	90	PRGFPGIQGRKGEPEGAYVYRSAFSVGLETYVTVPNMPIRFTTKIFYNQNHHDGSGTKF	149
Query:	147	TCPMPGVYFFAYHV	160
		C +PG+Y+FAYH+	
Sbjct:	150	HCNIPGLYYFAYHI	163

FIG. 23



BLASTP ALIGNMENT OF SEQ ID NO: 355 WITH HUMAN ADIPONECTIN  
AMINO ACID SEQUENCE (SEQ ID NO: 404)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 355)  
Subject: AAY85144 13-MAR-2000 09-MAR-1999 20-JUN-2000 09-MAR-1999 Human  
adiponectin amino acid sequence. [Homo sapiens] (SEQ ID NO: 404)  
Length = 244

Score = 204 (76.9 bits), Expect = 6.3e-17, P = 6.3e-17

Identities = 54/134 (40%), Positives = 69/134 (51%)

Query: 37 PRGPGPDGAPASVPPFP-----PGAKGEVRRGKAGLRGPPPGPPRPGPPGPRGPPG 91  
P+G G A +P P PG G G G+ G +G PG GP+G GE G PG G

Sbjct: 32 PKG-ACTGWMAGIPGHPGHNGAPGRDGTGPGKEKGDPGLIGPKGDIGETGVPGAEG 90

Query: 92 PPG-PGPGGVA--PAAG-YVPRIAIFYAGLRPPHEGYEVL-RFDDVVTNVGNAYEAASGKF 146  
P G PG G P G YV R AF GL + + RF + N Y+ ++GKF

Sbjct: 91 PRGFPGIQGRKGEPEGAYVYRSAFSVGLEITYYTIPNMPERFTKIFYNQNHHDGSGTGKF 150

Query: 147 TCPMPGVYFFAYHV 160  
C +PG+Y+FAYH+

Sbjct: 151 HCNIPGLYYFAYHI 164

FIG. 24

BLASTP ALIGNMENT OF SEQ ID NO: 378 WITH ADIPONECTIN POLYPEPTIDE (SEQ ID NO: 402)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 378)  
 Subject: gi15213856 AF404407\_1 (AF404407) adiponectin [Macaca mulatta] (SEQ ID NO: 402)  
 Length = 243

Score = 297 (109.6 bits), Expect = 5.0e-26, P = 5.0e-26

Identities = 80/215 (37%), Positives = 113/215 (52%)

Query: 37 PRGPGPDGAPASVPPFP-----PGAKGEVGRRGKAGLRGPPGPPGPRGPPGPPG 91  
 P+G G A +P P PG G G G+ G +G PG GP+G GE G G G  
 Sbjct: 31 PKG-ACTGWMAGIPGHPGNGVPGRDGRDGTGPKGKGDPLIGPKGDTGETGVTGAEG 89

Query: 92 PPG-PCGGVA--PAAG-YVPRIAFYAGLRRPHEGYEV-LRFDDVVTNVGNAYEAASGKF 146  
 P G PG G P G YV R AF GL + +RF + N N Y+ ++GKF  
 Sbjct: 90 PRGFPGIQGRKGEPEGEGAYVYRSAFSVGLETYVTVPNMPIRFTKIFYNQNHYDGTGKF 149

Query: 147 TCPMPGVYFFAYHVLMRGGDGTSMWADLMKNGQVRASAIADQADQNDYDASNSVILHLDV 206  
 C +PG+Y+FAYH+ + D + L K + Q + N D AS SV+LHL+V  
 Sbjct: 150 HCNIPGLYYFAYHITVYMKD---VKVSLFKKDKAMLFYTDQYQENNVDQASGVLHLEV 206

Query: 207 GDEVFIKLDG-GKVHG--GNTNKYSTFSGFIIYPD 238  
 GD+V++++ G G+ +G + + STF+GF++Y D  
 Sbjct: 207 GDQVWLQVYGEGERNGLYADNDNDSTFTGFLLYHD 241

FIG. 25

# TEDECT "6645000T"

## BLASTP ALIGNMENT OF SEQ ID NO: 378 WITH HUMAN ADIPONECTIN AMINO ACID SEQUENCE (SEQ ID NO: 404)

Query: Adiponectin-Like Polypeptide (SEQ ID NO: 378)  
Subject: AAY85144 13-MAR-2000 09-MAR-1999 20-JUN-2000 09-MAR-1999 Human  
adiponectin amino acid sequence. [Homo sapiens] (SEQ ID NO: 404)  
Length = 244

Score = 310 (114.2 bits), Expect = 3.7e-28, P = 3.7e-28

Identities = 82/215 (38%), Positives = 115/215 (53%)

Query: 37 PRGPGPDGAPASVPPFP-----PGAKGEVGRRGKAGLRGPPGPPGPPGPPGPPGPPG 91  
P+G G A +P P PG G G G+ G +G PG GP+G GE G PG G  
Sbjct: 32 PKG-ACTGWMAGIPGHPGHNAGPRDGRDGTGKEKGDPLIGPKGDIGETGVPGAEG 90

Query: 92 PPG-PGPGGVA--PAAG-YVPRIAFYAGLRPRPHEGYEVL-RFDDVVTNVGNAYEAAAGKF 146  
P G PG G P G YV R AF GL + + RF + N N Y+ ++GKF  
Sbjct: 91 PRGFPGIQGRKGEPGEGAYVYRSAFSVGLETYTIPNMPERFTKIFYNQNNHYDGTGKF 150

Query: 147 TCPMPGVYFFAYHVLMRGGDGTSMWADLMKNGQVRASAIQADQNDYASNSVILHLDV 206  
C +PG+Y+FAYH+ + D + L K + Q + NYD AS SV+LHL+V  
Sbjct: 151 HCNIPGLYFAYHITVYMKD---VKVSLFKDKAMLFTYDQYQNNYDQASGSVLLHLEV 207

Query: 207 GDEVFIKLDG-GKVHG--GNTNKYSTFSGFIIYPD 238  
GD+V++++ G G+ +G + + STF+GF++Y D  
Sbjct: 208 GDQVWLQVYGEGERNGLYADNDNDSTFTGFLIYHD 242

FIG. 26